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OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 09:48:28 ; Search time 1166.08 Seconds
(without alignments)
11181.073 Million cell updates/sec

Title: US-09-922-895-4

Perfect score: 448
Sequence: 1 TAGTCAGATGCAGAAATTT.....CCCTGCTTAATGAAAGCTT 448

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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37: em_hcg_vrt:*
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39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	448	100.0	448	6	ARI64121	ARI64121 Sequence
2	448	100.0	448	6	AX030931	AX030931 Sequence
3	448	100.0	1717	6	AX334894	AX334894 Sequence
4	448	100.0	1717	6	HS051241	U51241 Human eosin
5	448	100.0	1915	6	BD006761	BD006761 Chemokine
6	448	100.0	5791	9	AF247361	AF247361 Homo sapi
7	448	100.0	197279	9	AC104439	AC104439 Homo sapi
8	448	100.0	220965	2	HSR312688	AJ312688 Homo sapi
9	380.4	84.9	1689	9	HS049727	U49727 Human C-C C
10	339.2	75.7	7201	6	AX345239	AX345239 Sequence
11	294.4	65.7	7201	6	AX345238	AX345238 Sequence
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15	48.4	10.8	349980	6	AX344574	AX344574 Sequence
16	47.4	10.6	168406	2	AC090770	AC090770 Homo sapi
17	47.4	10.6	168476	9	AC011260	AC011260 Homo sapi
18	47.4	10.6	170337	2	AP001378	AP001378 Homo sapi
19	46.8	10.4	7025	6	AX339179	AX339179 Sequence
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ALIGNMENTS

RESULT 1
LOCUS ARI64121 448 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 4 from patent US 6271347.
ACCESSION ARI64121
VERSION ARI64121.1 GI:16235067
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 448)
AUTHORS Daugherty,B.L., Demartino,J.A., Siciliano,S.J. and Springer,M.S.
TITLE Eosinophil ecotaxin receptor
JOURNAL Patent: US 6271347-A 4 07-AUG-2001;
FEATURES Location/Qualifiers

source 1..448
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Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 421 AGTTCTTCCCTGCTTAATGAAAAGCTT 448

RESULT 2
AX030931 448 bp DNA linear PAT 20-SEP-2000
LOCUS AX030931
DEFINITION Sequence 4 from Patent EP1012190.
ACCESSION AX030931
VERSION AX030931.1 GI:10278336
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 448)
AUTHORS Daugherty, B.L., Demartino, J.A., Siciliano, S.J. and Springer, M.S.
TITLE Bostimophil eotaxin receptor
JOURNAL Patent: EP 1012190-A 4 28-JUN-2000;
MERCK & CO INC (US)
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source 1..448
location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 155 a 98 c 70 g 125 t
ORIGIN

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Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 AGTTCTTCCCTGCTTAATGAAAAGCTT 448
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Db 421 AGTTCTTCCCTGCTTAATGAAAAGCTT 448

RESULT 3
AX334894 1717 bp DNA linear PAT 09-JAN-2002
LOCUS AX334894
DEFINITION Sequence 5403 from Patent WO0194629.
ACCESSION AX334894
VERSION AX334894.1 GI:18125613
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ehner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
JOURNAL Patent: WO 0194629-A 5403 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source 1..1717
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 434 a 428 c 351 g 504 t
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Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 TTGAAGCACTGAAATATACACAGCAGTAGAGTAGATGATGATACCTTAAGTCAATT 180
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Db 1390 TTGAAGCACTGAAATATACACAGCAGTAGAGTAGATGATGATACCTTAAGTCAATT 1449

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QY 301 TGGCGGTACAAAAAGGTAAGCTTTTATATTTTATACATTAACTTCAGCAGCTATTGA 360
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DB 1570 TGGCGGTACAAAAAGGTAAGCTTTTATATTTTATACATTAACTTCAGCAGCTATTGA 1629
QY 361 TATTAATTAACATTTTCACACATACATTAAGTACATTTTATTTTCTAATGTGCC 420
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DB 1630 TATTAATTAACATTTTCACACATACATTAAGTACATTTTATTTTCTAATGTGCC 1689
QY 421 AGTTCTTCCCTGCCTTAATGAAGAGCTT 448
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DB 1690 AGTTCTTCCCTGCCTTAATGAAGAGCTT 1717

RESULT 4
LOCUS HSU51241 1717 bp DNA linear PRI 09-OCT-1996
DEFINITION Human eosinophil eotaxin receptor (CKBR3) gene, complete cds.
ACCESSION U51241
VERSION U51241.1 GI:1480480
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1717)
AUTHORS Daugherty,B.L., Siciliano,S.J., Demartino,J.A., Malkowitz,L.,
Siroclina,A. and Springer,M.S.
TITLE Cloning, expression, and characterization of the human eosinophil
eotaxin receptor
JOURNAL J. Exp. Med. 183 (5), 2349-2354 (1996)
MEDLINE 96235044
PUBMED 8642344
REFERENCE 2 (bases 1 to 1717)
AUTHORS Daugherty,B.L.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-1996) Bruce L. Daugherty, Inflammation Research,
Merck Research Laboratories, R80W-107, P.O. Box 2000, Rahway, NJ
07065, USA

FEATURES
source Location/Qualifiers

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BASE COUNT 434 a 428 c 351 g 504 t
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Best Local Similarity 100.0%; Pred. No. 3.3e-88;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1390 TTGAAGACACTGAATATACACACAGCAGTAGCAGTAGATGTAGTACCTTAAGCTATT 1449
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DB 1450 ACCACAGGCGAGGGCGTGGGCGAGGCTACATCATCATCAACCCATAAAGAGAGCTTGGT 1509
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DB 1630 TATTAATTAACATTTTCACACATACATTAAGTACATTTTATTTTCTAATGTGCC 1689
QY 421 AGTTCTTCCCTGCCTTAATGAAGAGCTT 448
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DB 1690 AGTTCTTCCCTGCCTTAATGAAGAGCTT 1717

RESULT 5
LOCUS BD006761 1915 bp DNA linear PAT 31-JAN-2002
DEFINITION Chemokine receptors 88-2B [CCR-3] and 88c and antibodies thereof.
ACCESSION BD006761
VERSION BD006761.1 GI:18635132
KEYWORDS JP 2001029089-A/2.
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 1915)
AUTHORS Gary,P.W., Sheicart,V.L. and Rayport,C.J.
TITLE Chemokine receptors 88-2B [CCR-3] and 88c and antibodies thereof
JOURNAL Patent: JP 2001029089-A 2 06-FEB-2001;
ICOS CORP

COMMENT OS Unidentified
PN JP 2001029089-A/2
PD 06-FEB-2001
PF 16-MAY-2000 JP 2000143832
PR 20-DEC-1995 US 08/575967, 07-JUN-1996 US 08/661393 PI
PATRICK W GARY, VICOMI L, SHEICART, CARROLL J RAYPORT PC
C12N15/09,C07K14/715,C07K16/24,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12N5/10,C12N15/02,C12P21/02,C12P21/08,C13Q1/68,G01N33/15, PC
G01N33/50,
PC G01N33/53,G01N33/566//A61K39/395,A61K39/395,A61K45/00,
A61P7/02, PC A61P17/06,
PC A61P19/02,A61P29/00,A61P31/12,(C12P21/02,C12R1:91),C12N15/00,
PC C12N5/00,A61P29/00,A61P31/12,(C12P21/02,C12R1:91),C12N15/00,
PC C12N5/00,C12N15/00
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CC Topology: Linear;
FT key Location/Qualifiers
CDS 362..1426.

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Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1487 AAGCTTTCACACTCACCCTCTAAACAGTCTTCAAACTTCAGTGCACACTGAAGCTC 1546
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Db 1547 TTGAACACAGTGAATATACACAGCAGTAGAGATGATGATGATGATGATGATGAT 1606
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Db 1607 ACCACAGGCGAGGGGCTGGGCGACGCTACTCATCAACCTTAAAGAGAGAGCTTGGCT 1666
QY 241 TCTCTCTCTAAATGAGTTACCTACATTTTAATGACACCTGATGATGATGATGATGAT 300
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QY 421 AGTTCTTTCCCTGCTTATGTAAGAGCTT 448
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Db 1847 AGTTCTTTCCCTGCTTATGTAAGAGAGCTT 1874

RESULT 6
LOCUS AF247361 5791 bp DNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, complete cds.
ACCESSION AF247361
VERSION AF247361.1 GI:19110542
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 5791)
AUTHORS Vijh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
            Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
            for a Rare TATA-less Promoter Structure Conserved between
            Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
REFERENCE 2 (bases 1 to 5791)
AUTHORS Vijh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Substitution
JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S.
            Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD
            20850, USA

FEATURES
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QY 121 TTGAACACAGTGAATATATACACAGCAGTAGAGATGATGATGATGATGATGATGAT 180
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Db 5200 TTGAACACAGTGAATATATACACAGCAGTAGAGATGATGATGATGATGATGATGAT 5259
QY 181 ACCACAGGCGAGGGGCTGGGCGACGCTACTCATCAACCTTAAAGAGAGAGCTTGGCT 240
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Db 5260 ACCACAGGCGAGGGGCTGGGCGACGCTACTCATCAACCTTAAAGAGAGAGCTTGGCT 5319
QY 241 TCTCTCTCTAAATGAGTTACCTACATTTTAATGACACCTGAATGTTAGATTACTATA 300
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Db 5320 TCTCTCTCTAAATGAGTTACCTACATTTTAATGACACCTGAATGTTAGATTACTATA 5379
QY 301 TGGCGGTACAAAAGGTAATTTTATTTATTTATATACATTACTTACAGCAGCTATGTA 360
    |||||||
Db 5380 TGGCGGTACAAAAGGTAATTTTATTTATTTATATACATTACTTACAGCAGCTATGTA 5439
QY 361 TATTAATTAACATTTTTCACACATACATTAAGTTAACTTTTATTTTCTAATGTGCTT 420
    |||||||
Db 5440 TATTAATTAACATTTTTCACACATACATTAAGTTAACTTTTATTTTCTAATGTGCTT 5499
QY 421 AGTTCTTTCCCTGCTTATGTAAGAGAGCTT 448
    |||||||
Db 5500 AGTTCTTTCCCTGCTTATGTAAGAGAGCTT 5527

RESULT 7
LOCUS AC104439 197279 bp DNA linear PRI 20-JUN-2002
DEFINITION Homo sapiens chromosome 3 clone RP11-793B15, complete sequence.
ACCESSION AC104439 AC024739
VERSION AC104439.2 GI:21490240
KEYWORDS
SOURCE human.
```

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 197279)
 AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
 Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
 and Haugen, E.D.
 TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 197279)
 AUTHORS Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
 TITLE Direct Submission
 JOURNAL Submitted (11-DEC-2001) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 REFERENCE 3 (bases 1 to 197279)
 AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
 Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
 and Haugen, E.D.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUN-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 COMMENT On Jun 20, 2002 this sequence version replaced gi:17488621.
 ----- Genome Center
 Center: University of Washington Genome Center
 Center Code: UMG
 Web site: <http://www.genome.washington.edu>
 Contact: wgchtgs@u.washington.edu
 Drafting Center: WUGSC
 ----- Project Information
 Center project name: chr-3
 Center clone name: RP11-793E15 (bc0564)
 ----- Summary Statistics
 Sequencing vector: unknown; 52% of reads
 Sequencing vector: plasmid; 108752; 48% of reads
 Chemistry: Dye-terminator ET; 94% of reads
 Chemistry: Dye-terminator Big Dye; 6% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 197168 bases at least Q40
 Consensus quality: 197255 bases at least Q30
 Consensus quality: 197275 bases at least Q20
 Insert size: 197279; sum-of-contigs
 Quality coverage: 8.2x in Q20 bases; sum-of-contigs

 Overlapping Sequences:
 5': RP11-91E8 (UMGC:bc0216) AC026349
 3': CMD-2563A18 (UMGC:bc0730)

 Sequence Quality Assessment:
 This entry has been annotated with sequence quality
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the
 GenBank flat file format but are available as part
 of this entry's ASN.1 file.

 This sequence was finished as follows unless otherwise noted:
 all regions were either double-stranded or sequenced with an
 alternate chemistry or covered by high quality data (i.e., Phred
 quality >= 30); an attempt was made to resolve all sequencing
 problems, such as compressions and repeats; all regions were
 covered by at least one plasmid subclone or more than one M13
 subclone; and the assembly was confirmed by restriction digest.

 Sequence Validation:
 This sequence has been validated by Multiple Complete Digest
 fingerprinting. Comparison of the experimentally derived digest
 fragments with sequence-predicted fragments is given below.
 The electronically-digested sequence consists of both insert and
 vector, in order to accurately represent the entire circular BAC.
 Small fragments below a variable cutoff (approximately 400-800 bp)
 are not resolved in the fingerprint and hence do not appear

in the table. There are no significant remaining discrepancies
 between the experimental and predicted values. Uniquely ordered
 fragments are separated by dashed lines.

HindIII				BglII				EcoRI			
SedgMap	FgPrnt	SedgMap	FgPrnt	SedgMap	FgPrnt	SedgMap	FgPrnt	SedgMap	FgPrnt	SedgMap	FgPrnt
2687	2617	8949	8586	8696	8661	6382	6410	2067	2160	6	<800
512	<800	7846	7940	2742	2803	449	<800	3734	3895	5376	5324
2602	2763	1334	1301	1493	1478	2590	2617	2287	2309	823	835
8313	8291	1814	1918	1962	2002	1711	1683	691	<800	2900	2954
9821	9472	5477	5348	1484	1478	516	<800	305	<800	1005	995
8587	8291	25245	25541	1181	1171	7446	7581	3988	4121	18560	19002
2088	2075	1633	1598	3603	3579	2509	2617	631	<800	4943	5076
3519	3501	90	<800	3239	3241	26	<800	402	<800	953	995
925	933	3350	3490	1621	1615	98	<800	4577	4515	6827	6900
6409	6410	1229	1183	79	<800	1383	1376	4221	4331	16418	16263
16048	15829	3980	4121	3361	3241	1876	1877	2548	2497	872	881
4169	4068	674	<800	4220	4193	1674	1683	2332	2309	2848	2803
52	<800	11445	11045	2283	2318	5227	5082	5692	5632	3211	3241
15464	15829	1385	1414	4615	4632	14333	14296	608	<800	6823	6900
1026	1026	3930	3895	886	881	645	<800	1465	1414	2032	2002
6621	6410	2382	2497	8680	8661	8413	8291	747	<800	5163	5076

1401	1376	1951	2012	1547	1478
1512	1471	642	<800	7058	6900
5801	5644	21060	21003	1647	1615
3256	3278	3700	3666	2753	2803
3448	3501	1321	1301	162	<800
2738	2763	10705	10502	1078	1093
237	<800	3128	3317	2156	2173
6715	6823	183	<800	5077	5076
201	<800	3255	3490	154	<800
1002	1026	5653	5632	1571	1478
221	<800	3380	3317	219	<800
2854	2899	237	<800	520	<800
6998	7317	421	<800	1540	1478
1174	1145	2152	2160	1479	1478
7876	8291	249	<800	1613	1615
1911	1877	2599	2778	1399	1478
3899	3847	685	<800	9553	9383
5672	5644	41	<800	166	<800
1711	1683	388	<800	13615	13115
862	854	2500	2497	4731	46322
2368	2389	2889	2778	5159	5076
		178	<800	4503	4430
		6589	6728	6607	6900
		3836	3895	2766	2803

Query Match	100.0%;	Score 448;	DB 9;	length 197279;
Best Local Similarity	100.0%;	Pred. No. 2.2e-88;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	TAGGTCACATGCAGAAAAATTCCTCTAAAGAGGAAGACCAAGGAGATACCAACCAACATT	60
Db	191253	TAGGTCACATGCAGAAAAATTCCTCTAAAGAGGAAGACCAAGGAGATACCAACCAACATT	191312
QY	61	AAGCCTTCACACACTACCTCTAAAAACAGCTCCTTAAACTCCAGTGCACACTGAAGCTTC	120
Db	191313	AAGCCTTCACACACTACCTCTAAAAACAGCTCCTTAAACTCCAGTGCACACTGAAGCTTC	191372
QY	121	TTGAAGACACAGAAATATATACACACAGCAGTGTGAGTATGATGATGTCCTTAAGTGCATT	180
Db	191373	TTGAAGACACAGAAATATATACACACAGCAGTGTGAGTATGATGATGTCCTTAAGTGCATT	191432
QY	181	ACCACAGGCCAGAGGGGCTGGGCGAGGATCTCATCTCAACCTTAAAAAAGCAGAGCTTTGCT	240
Db	191433	ACCACAGGCCAGAGGGGCTGGGCGAGGATCTCATCTCAACCTTAAAAAAGCAGAGCTTTGCT	191492
QY	241	TCTCTCTTAAAAATGAGTACCTACATTTTATATGCACCCTGAATGTTGATAGTTACTATA	300
Db	191493	TCTCTCTTAAAAATGAGTACCTACATTTTATATGCACCCTGAATGTTGATAGTTACTATA	191552

Qy	301	TCGCCCTCAAAAAGCTAAACTTTTATATTTTATCATTAACCTTCAGCCAGCATTTGA	360
Db	191553	TCGCCCTCAAAAAGCTAAACTTTTATATTTTATCATTAACCTTCAGCCAGCATTTGA	191612
Qy	361	TATAAATAAACATTTCACACATACAAATAGTTAACTATTTATTTCTAATGTGCT	420
Db	191613	TATAAATAAACATTTCACACATACAAATAGTTAACTATTTATTTCTAATGTGCT	191672
Qy	421	AGTTCTTCCCGCTTAATGAAAAGCTT	448
Db	191673	AGTTCTTCCCGCTTAATGAAAAGCTT	191700

LOCUS	220965 bp	DNA	linear	HTG-15-MAY-2002
DEFINITION	HSAG312688			
SEQUENCING IN PROGRESS	Homo sapiens chromosome 3 clone RP6-32g23 map 3p21.3, ***			
	***, 26 ordered pieces.			

ACCESSION	AJ312688
VERSION	AJ312688.2
KEYWORDS	HTG; HTGS_PHASE2.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS
1 Kiss, H., Yang, Y., Kiss, C., Andersson, K., Klein, G., Imreh, S. and

Dumanski, J.P.	
The transcriptional map of the common eliminated region 1 (C3CER1)	

in 3p21.3
JOURNAL
Eur. J. Hum. Genet. 10 (1), 52-61 (2002)

MEDLINE	21906202
PUBMED	11896456

REFERENCE	2 (bases 1 to 220965)
AUTHORS	Kiss, H.

TITLE	Submitted (01-APR-2001)	Kiss H., Microbiology and Tumorbiology
Direct Submission		

Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
SWEDEN

COMMENT On Apr 5, 2001 this sequence version replaced gi:13548633.
The sequence is a consensus sequence of clone RP4-787c23 (1-140400

bp), clone RP6-32g73 (31212-220965 bp), clone RP6-146e1 (partially, 1-6600 bp) and clone RP6-188g11 (partially, 1-108303 bp). The sequencing contigs are in order and the gaps between them are represented by 100 Ns.

Contig 1: 1-11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp

Contig 4: 28448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp

Contig 7: 61679-97342 bp Contig 8: 97443-117655 bp Contig 9:

117756-118727 bp Contig 10: 118828-121834 bp Contig 11: 121935-127855 bp Contig 12: 127856-130867 bp

12: 1279556-129383 bp Contig 13: 129484-131747 bp Contig 14:

131848-132316 bp Contig 16: 134556-135527 bp Contig 17: 135527-136000 bp

17:
135628-189051 bp Contig 18: 189152-189476 bp Contig 19:

189577-191375 bp Contig 20: 191476-201473 bp Contig 21: 201574-202307 bp Contig 22: 202308-203035 bp

22: 202408-204878 bp Contig 23: 204979-213531 bp Contig 24:

213632-218109 bp Contig 25: 218210-219800 bp
213632-218109 bp Contig 26: 219901-220965 bp

* NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
* provided by the submittor.

Oy		301	TGCCGCTCAAAAGGTAAACTTTTATTTTATACATTTCAGCCGCAGCATGA	360
Dd	6397	TGTCGTTATAAAGCGTAATAATTTTTTATATTTATATATTATTTTAGTTAGTTATTTGA		6456
Oy	361	TATAATAAACAATTTCACACAAATACATAAGTTAACTATTTTATTTTCAATGGCCT	420	
Dd	6457	TATAATAAATAATTTTATATATAATAATAAGTTAACTATTTTATTTTAAATGTTT	6516	
Oy	421	AGTTCTTCCCTGCTTAATGAAGAAGCTT	448	
Dd	6517	AGTTTTTTTTTGTTTAAATGAAGAAGCTT	6544	
RESULT 12				
LOCUS	AC095857			
DEFINITION	Rattus norvegicus clone CH230-10B21, *** SEQUENCING IN PROGRESS			
ACCESSION	AC095857			
VERSION	AC095857.6 GI:22474823			
KEYWORDS	HTG; PHAGE.SEL.			
SOURCE	Norway rat.			
ORGANISM	Rattus norvegicus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
	Rattus.			
REFERENCE	1 (bases 1 to 3202)			
AUTHORS	Muzny,D.,Marie, Metzker,M.,Lee, Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalibechi,Y., Aoyagi,A., Ayodeji,M., Bace,E., Baden,H., Baldini,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalto,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,J., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Evans,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Frisler,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Georgegeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guerrero,W., Gunaratne,P., Haaland,W., Hamli,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Huilyk,S., Humm,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolyet,A., Kapachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovac,C., Kovaic,S., Kraft,C.L., Lebow,H., Levin,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensheva,L., Louised,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahrlandtine,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mathliney,S., McLeod,M., McNeill,T., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Mundasa,M., Murphy,M., Nair,L., Nankevici,C., Neal,D., Neuton,N., Nguyen,N., Norris,S., Nwakellemen,O., Okwonu,G., Olarinpusagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Plankoch,C., Plopper,F., Polidexter,A., Popovic,K.D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Rellly,B., Rellly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodney,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shelly,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Somaj,D., Steed,A., Sodergren,E., Song,X.-Z., Sorrelle,R., Soosa,J., Steele,M., Strong,R., Sutton,A., Svatek,A., Tabors,P., Taylor,C., Taylor T., Thomas,N., Thomas,S., Tingey,A., Trejos Z., Usmali,K., Valas,R., Vera V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,J., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.			

```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

-----
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GDQA
Center clone name: CH230-10B21

----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 239947 bases at least Q40
Consensus quality: 250769 bases at least Q20
Consensus quality: 259279 bases at least Q20

-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draift_data.html)
* NOTE: This is a "working draft" sequence. It currently
* consists of 109 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
1021: contig of 1021 bp in length
1022 1121: gap of unknown length
1122 2717: contig of 1596 bp in length
2718 2817: gap of unknown length
2818 4081: contig of 1264 bp in length
4082 4181: gap of unknown length
4182 5449: contig of 1268 bp in length
5450 5549: gap of unknown length
5550 7262: contig of 1713 bp in length
7263 7362: gap of unknown length
7363 8704: contig of 1342 bp in length
8705 8804: gap of unknown length
8805 10409: contig of 1605 bp in length
10410 10509: gap of unknown length
10510 11717: contig of 1208 bp in length
11718 11817: gap of unknown length
11818 12933: contig of 1116 bp in length
12934 13033: gap of unknown length
13034 14530: contig of 1497 bp in length
14531 14630: gap of unknown length
14631 15906: contig of 1276 bp in length
15907 16006: gap of unknown length
16007 17545: contig of 1339 bp in length
17546 17645: gap of unknown length
17646 19259: contig of 1614 bp in length
19260 19359: gap of unknown length
19360 20931: contig of 1572 bp in length
20932 21031: gap of unknown length
21032 22282: contig of 1251 bp in length
22282

```

Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X.,
Zhuo, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R.,
Holt, R. A., Smith, H. O., Weinstein, G. and Gibbs, R. A.
Direct Submission
Unpublished
2 (bases 1 to 320202)
Worley, K.C.
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 320202)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 24, 2002 this sequence version replaced gi:22450501.
Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GDQA
Center clone name: CH230-10B21
Summary Statistics
Sequencing vector: Plasmid:
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 239947 bases at least Q40
Consensus quality: 250769 bases at least Q30
Consensus quality: 259279 bases at least Q20
NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_drift_data.html)
NOTE: This is a "working draft" sequence. It currently
consists of 109 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1
1021: contig of 1021 bp in length
1022
1121: gap of unknown length
1122
2717: contig of 1596 bp in length
2718
2817: gap of unknown length
2818
4081: contig of 1264 bp in length
4082
4181: gap of unknown length
4182
5449: contig of 1268 bp in length
5450
5549: gap of unknown length
5550
7262: contig of 1713 bp in length
7263
7362: gap of unknown length
7363
8704: contig of 1342 bp in length
8705
8804: gap of unknown length
8805
10409: contig of 1605 bp in length
10410
10509: gap of unknown length
10510
11171: contig of 1208 bp in length
11178
11817: gap of unknown length
11818
12933: contig of 1116 bp in length
12934
13033: gap of unknown length
14530
14530: contig of 1497 bp in length
14531
14630: gap of unknown length
14631
15906: contig of 1276 bp in length
15907
16006: gap of unknown length
16007
17545: contig of 1539 bp in length
17546
17645: gap of unknown length
17646
19259: contig of 1614 bp in length
19260
19359: gap of unknown length
19360
20931: contig of 1572 bp in length
21031
21031: gap of unknown length
22032
22282: contig of 1251 bp in length

[illegible]

LOCUS	1440 bp	DNA	linear	ROD 27-FEB-1996
DEFINITION	Mus musculus macrophage inflammatory protein-1 alpha receptor-like			
ACCESSION	2 gene, complete cds.			
VERSION	U28406			
KEYWORDS	U28406.1 GI:1203800			
SOURCE	Mus musculus.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 1440)			
TITLE	Gao,J.-L. and Murphy,P.M.			
JOURNAL	Cloning and differential tissue-specific expression of three mouse			
MEDLINE	beta chemokine receptor-like genes, including the gene for a			
REFERENCE	functional macrophage inflammatory protein-1 alpha receptor			
AUTHORS	J. Biol. Chem. 270 (29), 17494-17501 (1995)			
TITLE	95340546			
JOURNAL	7542241			
MEDLINE	2 (bases 1 to 1440)			
REFERENCE	Gao,J.-L.			
AUTHORS	Direct Submission			
TITLE	Submitted (05-JUN-1995) Ji-Liang Gao, Lab of Host Defenses, NIAID,			
JOURNAL	National Institutes of Health, Building 10, Room 11N113, Bethesda,			
COMMENT	MD 20892, USA			
FEATURES	On Feb 27, 1996 this sequence version replaced gi:1199860.			
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gene	1..1440			
CDs	/organism="Mus musculus"			
	/db_xref="taxon:10090"			
	/chromosome="9"			
	/clone_id="lambda FIX 129/Svj mouse genomic DNA library"			
	227..1350			
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	receptor-like 2 gene"			
	227..1306			
	/gene="macrophage inflammatory protein-1 alpha			
	receptor-like 2 gene"			
	/note="MP-1 alpha receptor like-2"			
	/protein_id="AA89155.1"			
	/db_xref="GI:1203801"			
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BASE COUNT	365	a	325	c	295	g	455	t	LPGEXMERTSSVSPSTGGEQLSVVF"
ORIGIN									
Query Match					12.5%;	Score 56.2;	DB 10;	Length 1440;	
Best Local Similarity					65.6%;	Pred. No. 0.022;			
Matches	82;	Conservative	0;	Mismatches	43;	Indels	0;	Gaps	0;
QY	13	AGAAATATGGCTTAAGAGAGACGACCAGGAGATGATTAACCAAAACACATTAAAGCTTCCACA	72						
Db	1315	AGAAATATGGCTACTTATTTCACATGACCTGAAGATGATTAACCAAAACACATTAAAGCTACACACA	1374						
QY	73	CTCACCCTCTAAACAGAGCTCTCAAACTCCAGTGCAGCACTGGAAGCTCTGGAGACACTG	132						
Db	1375	ATGACCTCTAGCTCAGTCATTTGTACTTTCCATGCATATGCTGATGCTCTCCAAAGACCTGT	1434						
QY	133	AAATTA	137						
Db	1435	AAACA	1439						

RESULT 15	AX344574/c	349980 bp	DNA	linear	PAT 01-FEB-2002
LOCUS	AX344574				
DEFINITION	Sequence 25 from Patent WO0200932.				
ACCESSION	AX344574				
VERSION	AX344574.1				
KEYWORDS	GI:18492460				
SOURCE	synthetic construct.				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Olek, A., Piepenbrock, C. and Berlin, R.				
TITLE	Diagnosis of known genetic parameters within the mhc				
JOURNAL	Patent: WO 0200932-A 25 03-JAN-2002; Epigenomics AG (DE)				
FEATURES	Location/Qualifiers				
Source	1..349980 /organism="synthetic construct" /db_xref="taxon:32630" /note="Chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3,673,778 <223>-split as follows -seq 01 0,000,001 TO 0,349,980-seq 02 0,300,001 649,980-seq 03 600,001 949,980-seq 04 900,001 1,249,980-seq 05 1,200,001 1,549,980-seq 06 1,500,001 1,849,980-seq 07 1,800,001 2,149,980-seq 08 2,100,001 2,449,980-seq 09 2,400,001 2,749,980-seq 10 2,700,001 3,049,980-seq 11 3,000,001 3,349,980-seq 12 3,300,001 3,649,980-seq 13 3,600,001 3,673,778 <223>-original length of seq 2: 3,673,778 <223>-split as follows -seq 14 0,000,001 TO 0,349,980-seq 15 0,300,001 649,980-seq 16 600,001 949,980-seq 17 900,001 1,249,980-seq 18 1,200,001 1,549,980-seq 19 1,500,001 1,849,980-seq 20 1,800,001 2,149,980-seq 21 2,100,001 2,449,980-seq 22 2,400,001 2,749,980-seq 23 2,700,001 3,049,980-seq 24 3,000,001 3,349,980-seq 25 3,300,001 3,649,980-seq 26 3,600,001 3,673,778"				
BASE COUNT	92483 a 4329 c 79047 g 174121 t				
ORIGIN					
Query Match	10.8%: Score 48.4; DB 6; Length 349980;				
Best Local Similarity	45.5%: Pred. No. 0.7;				
Matches 172; Conservative 0; Mismatches 206; Indels 0; Gaps 0;					
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Oy 75	CACCTCTAAACAGCTCTCAACTCCAGTCGACACTGAAGCTCTTGAGACACTGAA 134				
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QY 315 GGTAAACTTTTATATTTTATACATTAACCTCAGCCAGCTATTGATATATAATAAACAT 374
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Job time : 1751.75 secs